

**CRF Errors Edited by the STIC Systems  
Branch**

Serial Number: 10/539,396

CRF Edit Date: 6/29/05  
Edited by: sz

\_\_\_ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

\_\_\_ Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

\_\_\_ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

\_\_\_ Deleted:   /   invalid beginning/end-of-file text ; \_\_\_ page numbers

\_\_\_ Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

\_\_\_ Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

\_\_\_ Other:

\_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_



PCT

## RAW SEQUENCE LISTING

DATE: 06/29/2005

PATENT APPLICATION: US/10/539,396

TIME: 16:08:31

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06292005\J539396.raw

```

3 <110> APPLICANT: Tang, Lan
4      Wu, Wenping
5      Duan, Junxin
6      Johannesen, Pia Francke
8 <120> TITLE OF INVENTION: Thermostable alpha-amylases
10 <130> FILE REFERENCE: 10348.204-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/539,396
C--> 12 <141> CURRENT FILING DATE: 2005-06-16
12 <160> NUMBER OF SEQ ID NOS: 6
14 <170> SOFTWARE: PatentIn version 3.3
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 18
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Primer AM298-CDSF
24 <400> SEQUENCE: 1
25 tatcatgaaa ttcagcat                                     18
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 19
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Primer AM298-CDSR
36 <400> SEQUENCE: 2
37 agttcaaaat ggacaaagt                                     19
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 1438
42 <212> TYPE: DNA
43 <213> ORGANISM: Rhizomucor pusillus
46 <220> FEATURE:
47 <221> NAME/KEY: CDS
48 <222> LOCATION: (5)..(1417)
50 <220> FEATURE:
51 <221> NAME/KEY: sig_peptide
52 <222> LOCATION: (5)..(68)
54 <220> FEATURE:
55 <221> NAME/KEY: mat_peptide
56 <222> LOCATION: (68)..()
58 <400> SEQUENCE: 3
59 tatc atg aaa ttc agc atc tct ctc tcg gca gca att gta ctc ttc gcg   49
60      Met Lys Phe Ser Ile Ser Leu Ser Ala Ala Ile Val Leu Phe Ala
61      -20                -15                -10

```

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63 gcc gca aca agc ctt gca agc cct ttg ccc caa cag cag cga tat ggc      97
64 Ala Ala Thr Ser Leu Ala Ser Pro Leu Pro Gln Gln Gln Arg Tyr Gly
65   -5          -1 1          5          10
67 aaa aga gca act tcg gat gac tgg aaa agc aag gcc att tat cag ctg      145
68 Lys Arg Ala Thr Ser Asp Asp Trp Lys Ser Lys Ala Ile Tyr Gln Leu
69          15          20          25
71 ctt aca gat cga ttt ggc cgc gcc gat gac tca aca agc aac tgc tct      193
72 Leu Thr Asp Arg Phe Gly Arg Ala Asp Asp Ser Thr Ser Asn Cys Ser
73          30          35          40
75 aat tta tcc aac tac tgt ggt ggt acc tac gaa ggc att acg aag cat      241
76 Asn Leu Ser Asn Tyr Cys Gly Gly Thr Tyr Glu Gly Ile Thr Lys His
77          45          50          55
79 ctt gac tac att tcc ggt atg ggc ttt gat gct atc tgg ata tcg cca      289
80 Leu Asp Tyr Ile Ser Gly Met Gly Phe Asp Ala Ile Trp Ile Ser Pro
81          60          65          70
83 att ccc aag aac tcg gat gga ggc tac cac ggc tac tgg gct aca gat      337
84 Ile Pro Lys Asn Ser Asp Gly Gly Tyr His Gly Tyr Trp Ala Thr Asp
85 75          80          85          90
87 ttc tac caa cta aac agc aac ttt ggt gat gaa tcc cag ctc aaa gcg      385
88 Phe Tyr Gln Leu Asn Ser Asn Phe Gly Asp Glu Ser Gln Leu Lys Ala
89          95          100          105
91 ctc atc cag gct gcc cat gaa cgt gac atg tat gtt atg ctt gat gtc      433
92 Leu Ile Gln Ala Ala His Glu Arg Asp Met Tyr Val Met Leu Asp Val
93          110          115          120
95 gta gcc aat cat gca ggt ccc acc agc aat ggc tac tcg ggt tac aca      481
96 Val Ala Asn His Ala Gly Pro Thr Ser Asn Gly Tyr Ser Gly Tyr Thr
97          125          130          135
99 ttc ggc gat gca agt tta tat cat cct aaa tgc acc ata gat tac aat      529
100 Phe Gly Asp Ala Ser Leu Tyr His Pro Lys Cys Thr Ile Asp Tyr Asn
101          140          145          150
103 gat cag acg tct att gag caa tgc tgg gtt gct gac gag ttg cct gat      577
104 Asp Gln Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Glu Leu Pro Asp
105 155          160          165          170
107 att gac act gaa aat tct gac aac gtg gcc att ctc aac gac atc gtc      625
108 Ile Asp Thr Glu Asn Ser Asp Asn Val Ala Ile Leu Asn Asp Ile Val
109          175          180          185
111 tcc ggc tgg gtg ggt aac tat agc ttt gac ggc atc cgc att gat act      673
112 Ser Gly Trp Val Gly Asn Tyr Ser Phe Asp Gly Ile Arg Ile Asp Thr
113          190          195          200
115 gtc aag cat att cgc aag gac ttt tgg aca ggc tac gca gaa gct gcc      721
116 Val Lys His Ile Arg Lys Asp Phe Trp Thr Gly Tyr Ala Glu Ala Ala
117          205          210          215
119 ggc gta ttc gca act gga gag gtc ttc aat ggt gat ccg gcc tac gtt      769
120 Gly Val Phe Ala Thr Gly Glu Val Phe Asn Gly Asp Pro Ala Tyr Val
121          220          225          230
123 gga cct tat caa aag tac ctg cca tct ctc atc aat tac cca atg tat      817
124 Gly Pro Tyr Gln Lys Tyr Leu Pro Ser Leu Ile Asn Tyr Pro Met Tyr
125 235          240          245          250
127 tac gct ttg aac gac gtc ttt gta tcc aaa agc aaa gga ttc agc cgc      865

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128 Tyr Ala Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg
129                255                260                265
131 atc agc gaa atg cta gga tca aat cgc aat gcg ttt gag gat acc agc      913
132 Ile Ser Glu Met Leu Gly Ser Asn Arg Asn Ala Phe Glu Asp Thr Ser
133                270                275                280
135 gta ctt aca acg ttt gta gac aac cat gac aat ccg cgc ttc ttg aac      961
136 Val Leu Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn
137                285                290                295
139 agt caa agc gac aag gct ctc ttc aag aac gct ctc aca tac gta ctg      1009
140 Ser Gln Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu
141                300                305                310
143 cta ggt gaa ggc atc cca att gtg tat tat ggt tct gag caa ggt ttc      1057
144 Leu Gly Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe
145 315                320                325                330
147 agc gga gga gcg gat cct gct aac cgt gaa gtg ctg tgg acc acc aat      1105
148 Ser Gly Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Thr Asn
149                335                340                345
151 tat gat aca tcc agc gat ctc tac caa ttt atc aag aca gtc aac agt      1153
152 Tyr Asp Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser
153                350                355                360
155 gtc cgc atg aaa agc aac aag gcc gtc tac atg gat att tat gtt ggc      1201
156 Val Arg Met Lys Ser Asn Lys Ala Val Tyr Met Asp Ile Tyr Val Gly
157                365                370                375
159 gac aat gct tac gcc ttc aag cac ggc gat gct ttg gtt gtt ctc aat      1249
160 Asp Asn Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn
161                380                385                390
163 aac tat gga tca ggt tcc aca aac caa gtc agc ttc agc gtt agt ggc      1297
164 Asn Tyr Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly
165 395                400                405                410
167 aag ttc gat agc ggc gca agc ctc atg gat att gtc agt aac att acc      1345
168 Lys Phe Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr
169                415                420                425
171 acc acg gtg tcc tcg gat gga aca gtc act ttc aac ctt aaa gat gga      1393
172 Thr Thr Val Ser Ser Asp Gly Thr Val Thr Phe Asn Leu Lys Asp Gly
173                430                435                440
175 ctt ccg gct atc ttc acc tct gct taactttgtc cattttgaac t      1438
176 Leu Pro Ala Ile Phe Thr Ser Ala
177                445                450
180 <210> SEQ ID NO: 4
181 <211> LENGTH: 471
182 <212> TYPE: PRT
183 <213> ORGANISM: Rhizomucor pusillus
185 <400> SEQUENCE: 4
187 Met Lys Phe Ser Ile Ser Leu Ser Ala Ala Ile Val Leu Phe Ala Ala
188 -20                -15                -10
191 Ala Thr Ser Leu Ala Ser Pro Leu Pro Gln Gln Gln Arg Tyr Gly Lys
192 -5                -1 1                5                10
195 Arg Ala Thr Ser Asp Asp Trp Lys Ser Lys Ala Ile Tyr Gln Leu Leu
196                15                20                25

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199 Thr Asp Arg Phe Gly Arg Ala Asp Asp Ser Thr Ser Asn Cys Ser Asn
200      30      35      40
203 Leu Ser Asn Tyr Cys Gly Gly Thr Tyr Glu Gly Ile Thr Lys His Leu
204      45      50      55
207 Asp Tyr Ile Ser Gly Met Gly Phe Asp Ala Ile Trp Ile Ser Pro Ile
208 60      65      70      75
211 Pro Lys Asn Ser Asp Gly Gly Tyr His Gly Tyr Trp Ala Thr Asp Phe
212      80      85      90
215 Tyr Gln Leu Asn Ser Asn Phe Gly Asp Glu Ser Gln Leu Lys Ala Leu
216      95      100      105
219 Ile Gln Ala Ala His Glu Arg Asp Met Tyr Val Met Leu Asp Val Val
220      110      115      120
223 Ala Asn His Ala Gly Pro Thr Ser Asn Gly Tyr Ser Gly Tyr Thr Phe
224      125      130      135
227 Gly Asp Ala Ser Leu Tyr His Pro Lys Cys Thr Ile Asp Tyr Asn Asp
228 140      145      150      155
231 Gln Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Glu Leu Pro Asp Ile
232      160      165      170
235 Asp Thr Glu Asn Ser Asp Asn Val Ala Ile Leu Asn Asp Ile Val Ser
236      175      180      185
239 Gly Trp Val Gly Asn Tyr Ser Phe Asp Gly Ile Arg Ile Asp Thr Val
240      190      195      200
243 Lys His Ile Arg Lys Asp Phe Trp Thr Gly Tyr Ala Glu Ala Ala Gly
244      205      210      215
247 Val Phe Ala Thr Gly Glu Val Phe Asn Gly Asp Pro Ala Tyr Val Gly
248 220      225      230      235
251 Pro Tyr Gln Lys Tyr Leu Pro Ser Leu Ile Asn Tyr Pro Met Tyr Tyr
252      240      245      250
255 Ala Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg Ile
256      255      260      265
259 Ser Glu Met Leu Gly Ser Asn Arg Asn Ala Phe Glu Asp Thr Ser Val
260      270      275      280
263 Leu Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn Ser
264      285      290      295
267 Gln Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu Leu
268 300      305      310      315
271 Gly Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe Ser
272      320      325      330
275 Gly Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Thr Asn Tyr
276      335      340      345
279 Asp Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser Val
280      350      355      360
283 Arg Met Lys Ser Asn Lys Ala Val Tyr Met Asp Ile Tyr Val Gly Asp
284      365      370      375
287 Asn Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn Asn
288 380      385      390      395
291 Tyr Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly Lys
292      400      405      410
295 Phe Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr Thr

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```

296          415          420          425
299 Thr Val Ser Ser Asp Gly Thr Val Thr Phe Asn Leu Lys Asp Gly Leu
300          430          435          440
303 Pro Ala Ile Phe Thr Ser Ala
304          445          450
307 <210> SEQ ID NO: 5
308 <211> LENGTH: 32
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Primer 168/R.p. amy3-forw
315 <400> SEQUENCE: 5
316 gaagatctac catgaaattc agcatctctc tc
319 <210> SEQ ID NO: 6
320 <211> LENGTH: 30
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Primer 169/R.p. amy4-rev
327 <400> SEQUENCE: 6
328 ccgctcgagt taagcagagg tgaagatagc

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/539,396

DATE: 06/29/2005

TIME: 16:08:32

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\06292005\J539396.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date